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TAGGCATAAATTGGTCTGCGCACCAGCACCATGCAACTTTTTTCACCTCTGCCTAATCATC
1  -----+-----+-----+-----+-----+ 60
ATCCGTATTTAACCAGACGCGTGGTCTGGTACGTTGAAAAAGTGGAGACGGATTAGTAG
a  * A * I G L R T S T M Q L F H L C L I I -
TCTTGTTTCATGTCCTACTGTTCAAGCCTCCAAGCTGTGCCTTGGGTGGCTTTGGGGCATG
61  -----+-----+-----+-----+-----+ 120
AGAACAAGTACAGGATGACAAGTTCGGAGGTTTCGACACGGAACCCACCGAAACCCCGTAC
a  S C S C P T V Q A S K L C L G W L W G M -
GACATCGACCCTTATAAAGAATTTGGAGCTACTGTGGAGTTACTCTCGTTTTTGCCTTCT
121  -----+-----+-----+-----+-----+ 180
CTGTAGCTGGGAATATTTCTTAAACCTCGATGACACCTCAATGAGAGCAAAAACGGAAGA
a  D I D P Y K E F G A T V E L L S F L P S -
GACTTCTTTTCCTTCAGTACGAGATCTTCTAGATACCGCCTCAGCTCTGTATCGGGAAGCC
181  -----+-----+-----+-----+-----+ 240
CTGAAGAAAGGAAGTCATGCTCTAGAAGATCTATGGCGGAGTCGAGACATAGCCCTTCGG
a  D F F P S V R D L L D T A S A L Y R E A -
TTAGAGTCTCCTGAGCATTGTTACCTCACCATACTGCACTCAGGCAAGCAATTCTTTGC
241  -----+-----+-----+-----+-----+ 300
AATCTCAGAGGACTCGTAACAAGTGGAGTGGTATGACGTGAGTCCGTTTCGTTAAGAAACG
a  L E S P E H C S P H H T A L R Q A I L C -
TGGGGGGAACTAATGACTCTAGCTACCTGGGTGGGTGTTAATTTGGAAGATCCAGCGTCT
301  -----+-----+-----+-----+-----+ 360
ACCCCCCTTGATTACTGAGATCGATGGACCCACCCACAATTAAACCTTCTAGGTTCGCAGA
a  W G E L M T L A T W V G V N L E D P A S -
AGAGACCTAGTAGTCAGTTATGTCAACACTAATATGGGCCTAAAGTTCAGGCAACTCTTG
361  -----+-----+-----+-----+-----+ 420
TCTCTGGATCATCAGTCAATACAGTTGTGATTATACCCGGATTTCAGTCCGTTGAGAAC
a  R D L V V S Y V N T N M G L K F R Q L L -
TGGTTTCACATTCTTGTCTCACTTTTGAAGAGAAACAGTTATAGAGTATTTGGTGTCT
421  -----+-----+-----+-----+-----+ 480
ACCAAAGTGTAAGAAGACAGAGTGAAAACCTTCTCTTTGTCAATATCTCATAAACCACAGA
a  W F H I S C L T F G R E T V I E Y L V S -
TTCGGAGTGTGGATTGCGACTCCTCCAGCTTATAGACCACCAAATGCCCTATCCTATCA
481  -----+-----+-----+-----+-----+ 540
AAGCCTCACACCTAAGCGTGAGGAGGTGCAATATCTGGTGGTTTACGGGGATAGGATAGT
a  F G V W I R T P P A Y R P P N A P I L S -
ACACTTCCGGAGACTACTGTTGTTAGACGACGAGGCAGGTCCCCTAGAAGAAGAACTCCC
541  -----+-----+-----+-----+-----+ 600
TGTGAAGGCCCTCTGATGACAACAATCTGCTGCTCCGTCCAGGGGATCTTCTTCTTGAGGG
a  T L P E T T V V R R R G R S P R R R T P -
TCGCCTCGCAGACGAAGGTCTCAATCGCCGCGTCGAGAAGATCTCAATCTCGGGAATCT
601  -----+-----+-----+-----+-----+ 660
AGCGGAGCGTCTGCTTCCAGAGTTAGCGGCGCAGCGTCTTCTAGAGTTAGAGCCCTTAGA
a  S P R R R R S Q S P R R R R S Q S R E S -
CAATGTTAG
661  ----- 669
GTTACAATC
a  Q C * -

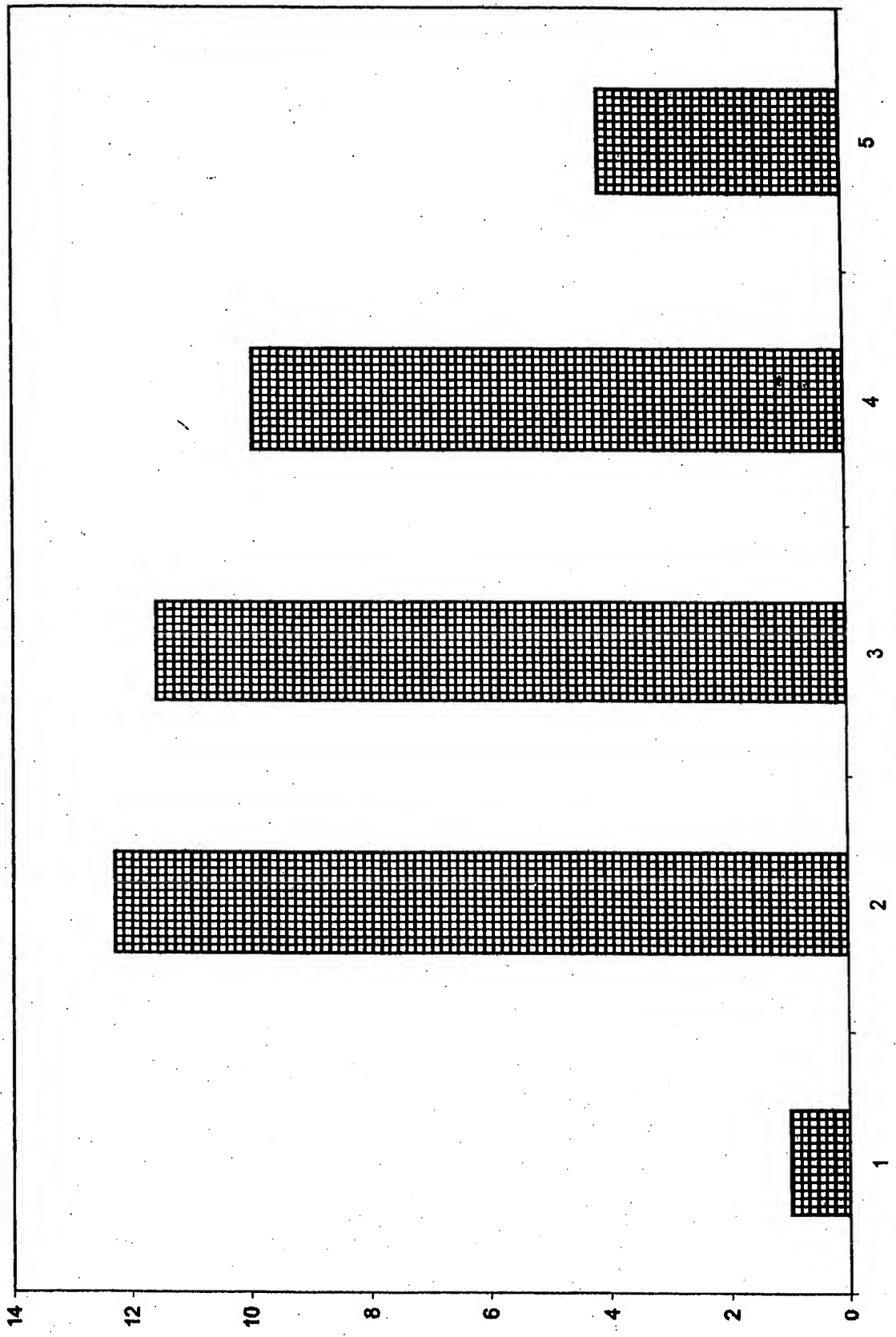
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Enzymes that do cut:

NONE

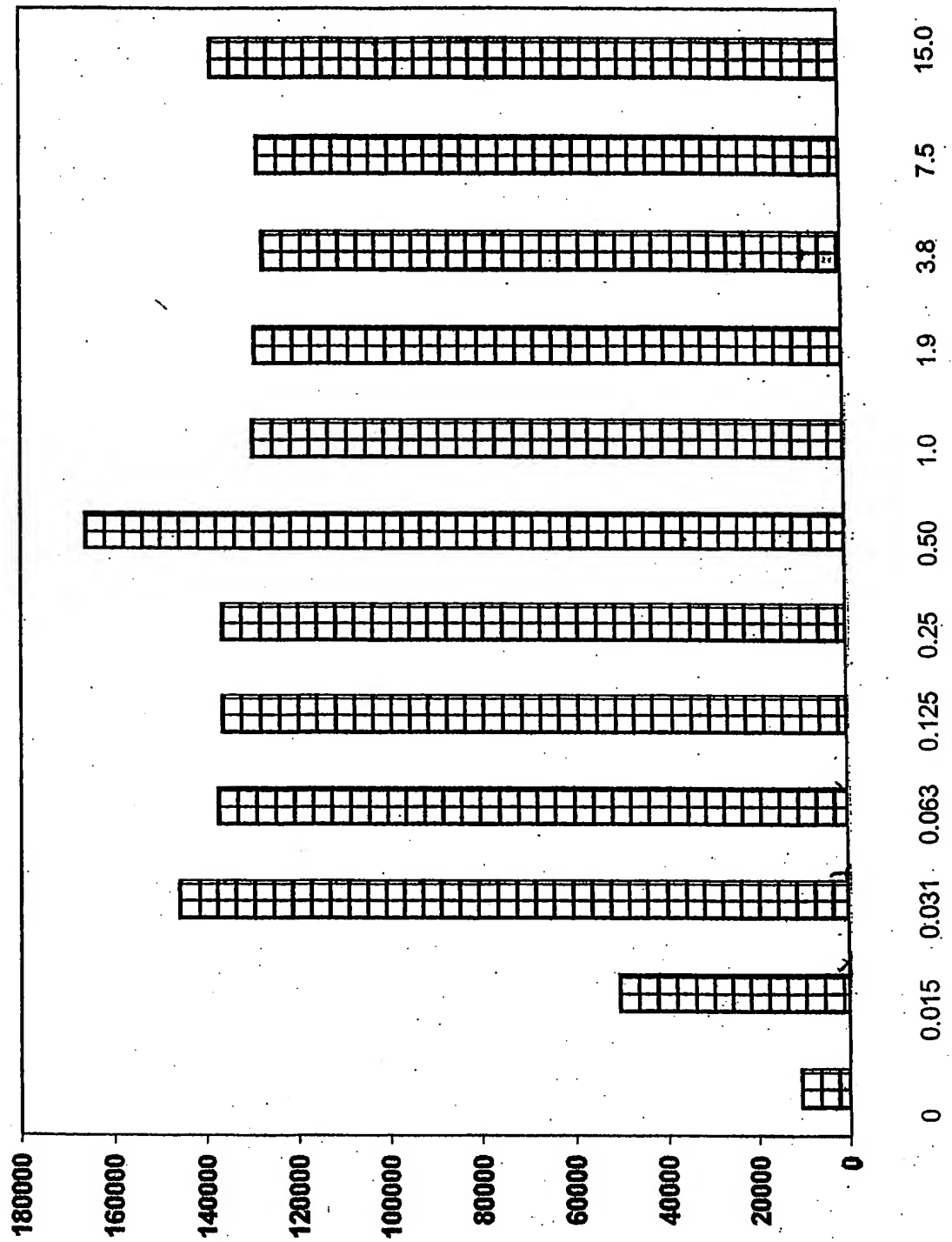
FIGURE 1

Figure 2



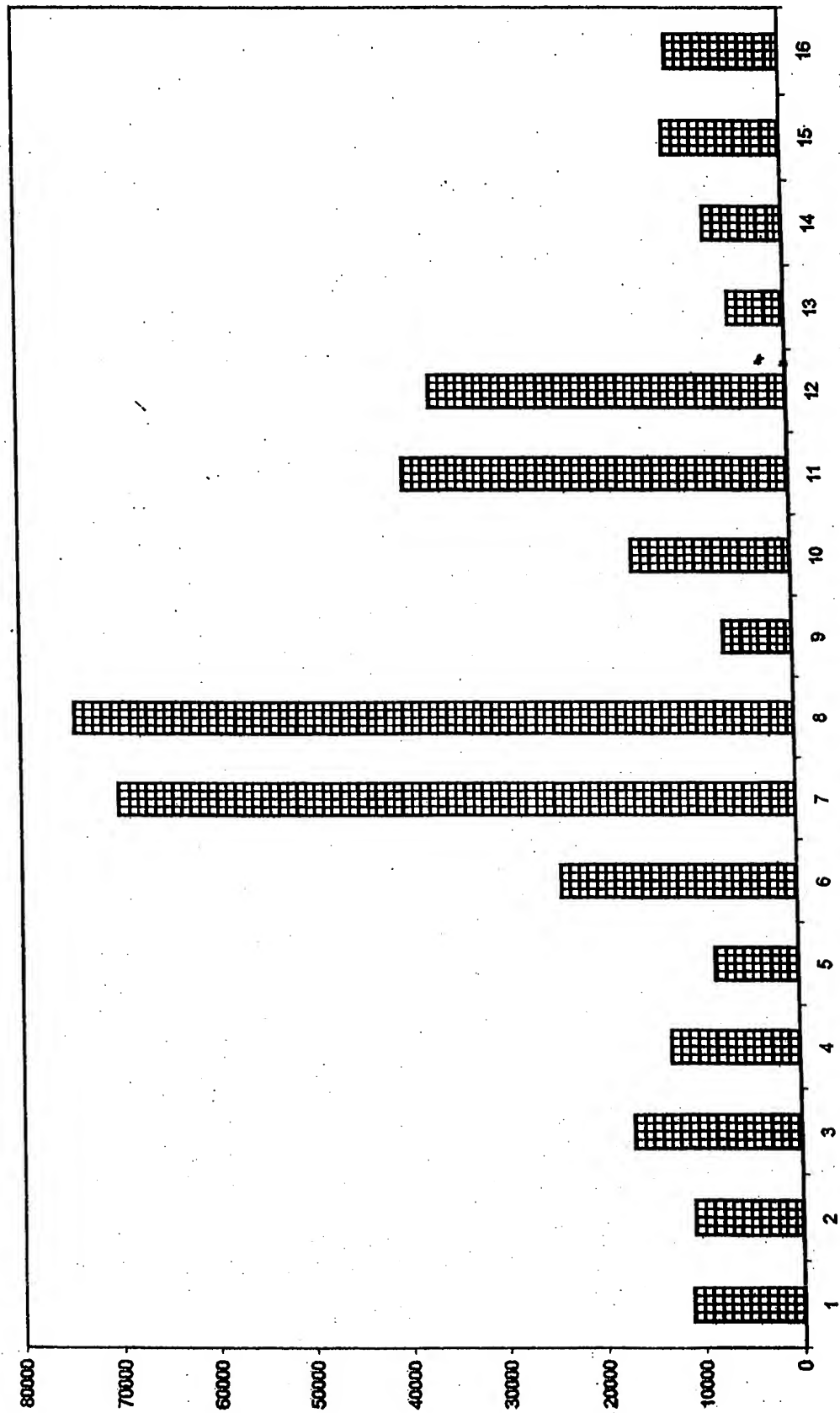
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Figure 3



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Figure 4a

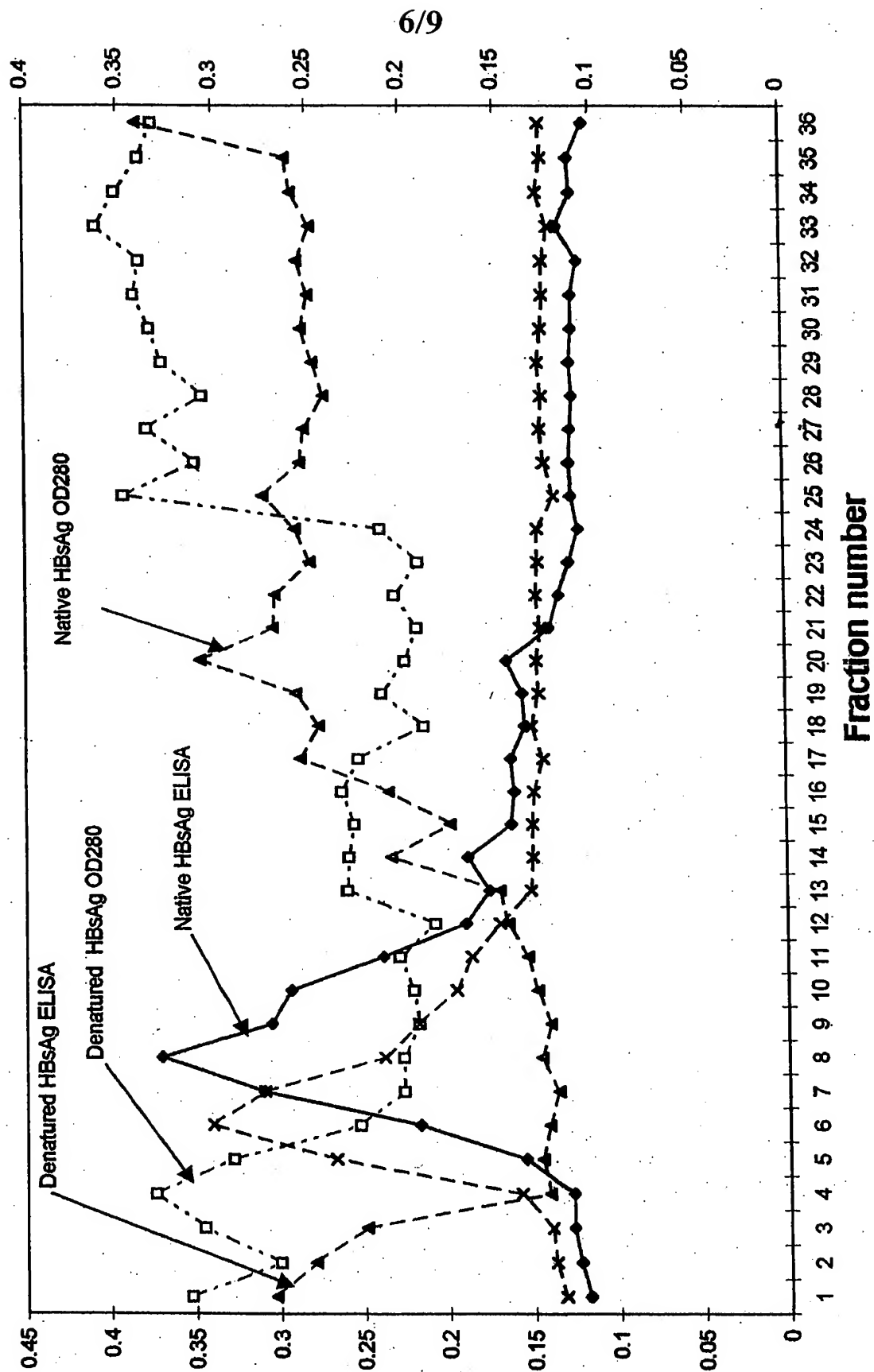


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Figure 4b

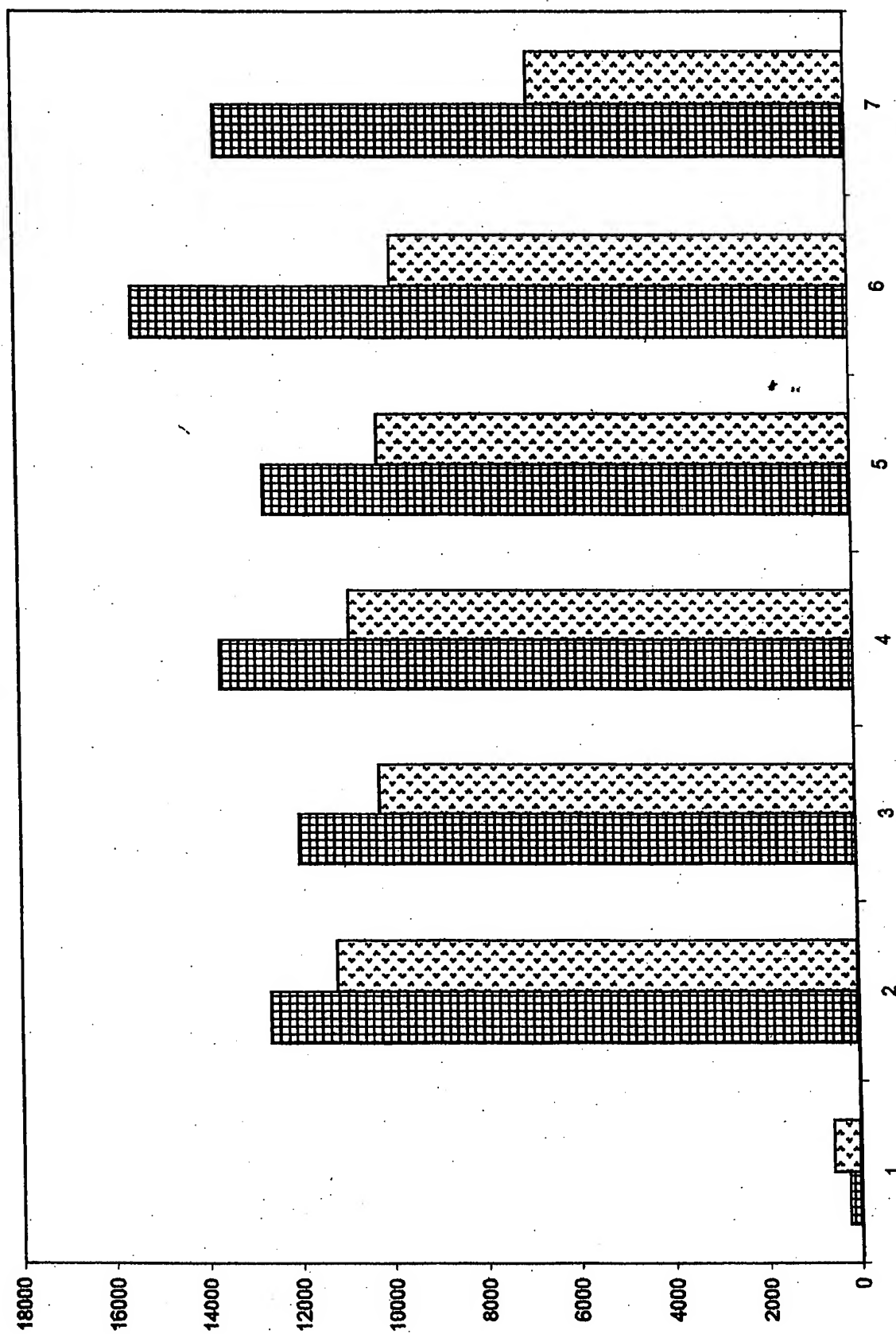
Treatment	day 2	day 3
Imm no ag	5096	11224
Imm 0.1 ug	5614	10904
Imm 1 ug	7266	16991
Imm 5 ug	5882	13120
Imm OT (3mg) no ag	4924	8409
Imm OT (3mg) 0.1 ug ag	7235	24250
Imm OT (3mg) 1 ug	14605	70078
Imm OT (3mg) 5 ag	11995	74585
Imm OT (1mg) no ag	3558	7079
Imm OT (1mg) 0.1 ug ag	4871	16339
Imm OT (1mg) 1 ug	4949	39954
Imm OT (1mg) 5 ag	4172	37059
Imm OT (0.1mg) no ag	5661	5904
Imm OT (0.1mg) 0.1 ug ag	12094	8168
Imm OT (0.1mg) 1 ug	23445	12242
Imm OT (0.1mg) 5 ag	36710	11754

Figure 5

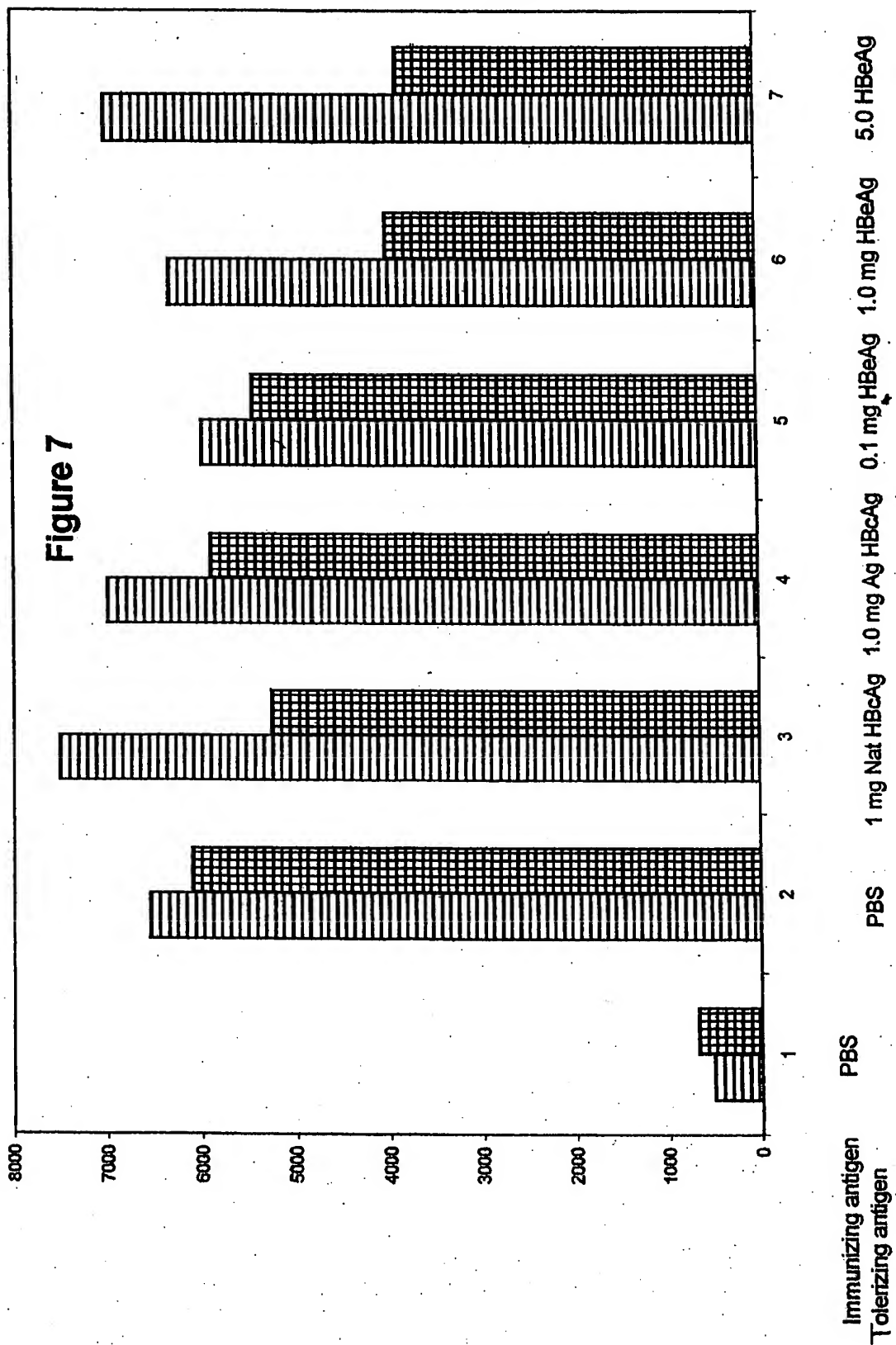


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Figure 6



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Figure 8

